

# Rehan Akbani

## List of Publications by Year in descending order

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86  
papers

58,369  
citations

22099

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docs citations

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times ranked

69098  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	13.9	4,139
2	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
3	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
4	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
5	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
6	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
7	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
8	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
9	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	13.7	2,149
10	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
11	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
12	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	13.5	1,718
13	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
14	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
15	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
16	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
17	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
18	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242

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19	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
20	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
21	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
22	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
23	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
24	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	2.9	683
25	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
26	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
27	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
28	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
29	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
30	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
31	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
32	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
33	A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014, 5, 3887.	5.8	456
34	TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013, 10, 1046-1047.	9.0	446
35	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3.	7.7	433
36	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	7.7	422

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37	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
38	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
39	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
40	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.	2.9	382
41	Tumour angiogenesis regulation by the miR-200 family. <i>Nature Communications</i> , 2013, 4, 2427.	5.8	363
42	TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D1018-D1022.	6.5	358
43	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
44	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
45	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
46	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , 2016, 14, 2476-2489.	2.9	298
47	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284
48	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
49	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
50	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
51	Characterization of Human Cancer Cell Lines by Reverse-phase Protein Arrays. <i>Cancer Cell</i> , 2017, 31, 225-239.	7.7	190
52	Realizing the Promise of Reverse Phase Protein Arrays for Clinical, Translational, and Basic Research: A Workshop Report. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1625-1643.	2.5	152
53	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ 2 Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
54	Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. <i>Clinical Cancer Research</i> , 2015, 21, 4514-4524.	3.2	110

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55	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- $\beta$ Pathway. <i>Gastroenterology</i> , 2018, 154, 195-210.	0.6	105
56	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	2.9	103
57	Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. <i>Cancer Research</i> , 2017, 77, e51-e54.	0.4	101
58	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
59	TCPA v3.0: An Integrative Platform to Explore the Pan-Cancer Analysis of Functional Proteomic Data. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S15-S25.	2.5	61
60	Using reverse-phase protein arrays as pharmacodynamic assays for functional proteomics, biomarker discovery, and drug development in cancer. <i>Seminars in Oncology</i> , 2016, 43, 476-483.	0.8	55
61	Development of a robust classifier for quality control of reverse-phase protein arrays. <i>Bioinformatics</i> , 2015, 31, 912-918.	1.8	43
62	Focal adhesion kinase. <i>Cancer Biology and Therapy</i> , 2014, 15, 919-929.	1.5	42
63	Large-Scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines. <i>Cancer Cell</i> , 2020, 38, 829-843.e4.	7.7	40
64	A Galaxy Implementation of Next-Generation Clustered Heatmaps for Interactive Exploration of Molecular Profiling Data. <i>Cancer Research</i> , 2017, 77, e23-e26.	0.4	32
65	EMLTrust: An enhanced Machine Learning based Reputation System for MANETs. <i>Ad Hoc Networks</i> , 2012, 10, 435-457.	3.4	31
66	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019, 8, 1750.	0.8	31
67	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019, 8, 1750.	0.8	31
68	Mobile Ad-Hoc Networks Security. <i>Lecture Notes in Electrical Engineering</i> , 2012, , 659-666.	0.3	28
69	HEAP: A packet authentication scheme for mobile ad hoc networks. <i>Ad Hoc Networks</i> , 2008, 6, 1134-1150.	3.4	24
70	A Comprehensive Comparison of Normalization Methods for Loading Control and Variance Stabilization of Reverse-Phase Protein Array Data. <i>Cancer Informatics</i> , 2014, 13, CIN.S13329.	0.9	19
71	Mutational Profiles Reveal an Aberrant TGF- $\beta$ -CEA Regulated Pathway in Colon Adenomas. <i>PLoS ONE</i> , 2016, 11, e0153933.	1.1	17
72	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	2.9	16

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73	Bayesian Hierarchical Varying-Sparsity Regression Models with Application to Cancer Proteogenomics. Journal of the American Statistical Association, 2019, 114, 48-60.	1.8	15
74	Personalized Integrated Network Modeling of the Cancer Proteome Atlas. Scientific Reports, 2018, 8, 14924.	1.6	14
75	Molecular heterogeneity at the network level: high-dimensional testing, clustering and a TCGA case study. Bioinformatics, 2017, 33, 2890-2896.	1.8	13
76	Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome. JCO Clinical Cancer Informatics, 2020, 4, 399-411.	1.0	13
77	Consensus subtypes of hepatocellular carcinoma associated with clinical outcomes and genomic phenotypes. Hepatology, 2022, 76, 1634-1648.	3.6	10
78	Analytical Platforms 3: Processing Samples via the RPPA Pipeline to Generate Large-Scale Data for Clinical Studies. Advances in Experimental Medicine and Biology, 2019, 1188, 113-147.	0.8	9
79	Identification and validation of a prognostic proteomic signature for cervical cancer. Gynecologic Oncology, 2019, 155, 324-330.	0.6	8
80	The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. European Urology Focus, 2015, 1, 94-95.	1.6	7
81	Enhancing role-based trust management with a reputation system for MANETs. Eurasip Journal on Wireless Communications and Networking, 2011, 2011, .	1.5	6
82	Credentialing Individual Samples for Proteogenomic Analysis. Molecular and Cellular Proteomics, 2018, 17, 1515-1530.	2.5	5
83	SAMMI: a semi-automated tool for the visualization of metabolic networks. Bioinformatics, 2020, 36, 2616-2617.	1.8	3
84	NExUS: Bayesian simultaneous network estimation across unequal sample sizes. Bioinformatics, 2020, 36, 798-804.	1.8	2
85	Generation of Raw RPPA Data and Their Conversion to Analysis-Ready Data. Advances in Experimental Medicine and Biology, 2019, 1188, 165-180.	0.8	2
86	Genomic Assessment of Muscle-Invasive Bladder Cancer: Insights from the Cancer Genome Atlas (TCGA) Project. Molecular Pathology Library, 2018, , 43-64.	0.1	0